

ACCESS DB # 153665  
PLEASE PRINT CLEARLY

FOR OFFICIAL USE ONLY

Scientific and Technical Information Center  
SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5-17-95  
Art Unit: 1635 Phone Number: 2-0762 Serial Number: 091486757  
Location (Bldg/Room#): 2028 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Cytochrome P 450 reductase  
Inventors (please provide full names): KUTCHAN et al.

Earliest Priority Date: 7/13/00

*CR/PC*

Search Topic:

*Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.*

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please Send Seq ID No: 10*

*PA 2649*

*No Anteference please.*

*No size limits*

*Thanks.*

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_

Type of Search

NA Sequence (#)

Vendors and cost where applicable

STN  Dialog

Searcher Phone #: \_\_\_\_\_

AA Sequence (#)

Questel/Orbit  Lexis/Nexis

Searcher Location: \_\_\_\_\_

Structure (#)

Westlaw  WWW/Internet

Date Searcher Picked Up: 5/20/05

Bibliographic

*Q3P*  In-house sequence systems

Date Completed: 5/23/05

Litigation

Commercial  Oligomer  Score/Length

Searcher Prep & Review Time: \_\_\_\_\_

Fulltext

Interference  SPDI  Encode/Transl

Online Time: \_\_\_\_\_

Other

Other (specify)

GenCore version 5.1.6  
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Om nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:00:17 ; Search time 8894 Seconds

(without alignments) 12172.472 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: cggcacgagttgttagat.....tttgagaaaaaaa 2649

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:  
1: /cgn2\_6/ptodata/1/pna/PCTRUS1\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/pna/PCTRUS2\_COMB.seq:\*

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116: /cgn2\_6/ptodata/1/pna/US6046\_COMB.seq:\*

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on:

May 22, 2005, 05:22:02 ; Search time 760 seconds  
(without alignments)  
7754.887 Million cell updates/sec

Title: US-09-486-757-10  
perfect score: 2649

Sequence: 1 cggcacagctgtttagat.....ttttggaaaaaaa 2649

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11689648 seqs, 1112441377 residues

Total number of hits satisfying chosen parameters: 23379296  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:/\*  
2: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:/\*  
3: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:/\*  
4: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:/\*  
5: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:/\*  
6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:/\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:/\*  
8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:/\*  
9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:/\*  
10: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:/\*  
11: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq:/\*  
12: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq:/\*  
13: /cgn2\_6/ptodata/1/pna/US11\_NEW\_COMB.seq:/\*  
14: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Rank	Rank
1	11689648	1	1

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 GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

May 22, 2005, 08:25:35

Search time 1432 Seconds  
 (without alignment)  
 11343.938 Million cell updates/sec

Title: US-09-486-757-10

Perfect score:

2649

Sequence:

1 cggccgcgagcttggat.....ttttggaaaaaaa 2649

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched:

5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications №:\*

```

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match Length	DB ID	Description
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 04:40:28 ; Search time 455 Seconds  
(without alignments) 9526.367 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggccacgagttgttagat.....tttgagaaaaaaaaaa 2649

Scoring table: IDENTITY\_NUC

Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Issued Patients NA:\*

1: /cgmn2\_6/ptodata/1/ina/5A COMB.seq: \*  
2: /cgmn2\_6/ptodata/1/ina/5B COMB.seq: \*  
3: /cgmn2\_6/ptodata/1/ina/6A COMB.seq: \*  
4: /cgmn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgmn2\_6/ptodata/1/ina/PC11US COMB.seq: \*  
6: /cgmn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# Query No. Score Match Length DB ID Description

GenCore Version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 00:44:41 ; Search time 1305 Seconds  
 (without alignments)  
 12016.394 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggacgagtttttagat.....tttttagaaaaaaa 2649

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390205 seqs, 2359870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003ab:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
------------	-------	--------------------	-------	-------------



ORIGIN	QY	841	GAGGATGCTGCCCTCAGGGCTACACCTATATGCTACTGCTGCTGATAACGGTA
	Db	841	GAGGATGCTGCCCTCAGGGCTACACCTATATGCTACTGCTGCTGATAACGGTA
	QY	901	GTGATTACCGAACATCGGTCGCGCTCTGGATGATAAACCATATACTGCTAACGGC
	Db	901	GTGATTACCGAACATCGGTCGCGCTCTGGATGATAAACCATATACTGCTAACGGC
	QY	961	GATGTCGATTGATTCTCATCTTGAGAACCATGGTCACAAAGAGAGCTC
	Db	961	GATGTCGATTGATTCTCATCTTGAGAACCATGGTCACAAAGAGAGCTC

Query Match	99.9%	Score 2645.8;	DB 8;	Length 2650;
Best Local Similarity	99.9%	Pre. No. 0;	0;	Mismatches
Matches 2647;	Conservative	2;	Indels 0;	Gaps 0;
QY	1 CGGCAAGGCTTGTAGTACCTCTAGGTGAAAGAGCAGGAGGAGAAAGT 60	Db	1021 CACAAACCAAGTCTATAGTCCTATACCTCGAGTTGACATATCGGCCTCTC 1080	
Db	1 CGGCAAGGCTTGTAGTACCTCTAGGTGAAAGAGCAGGAGGAGAAAGT 60	QY	1081 CTTACATATGAGACTCGGAGATCATCTTGTTTATGCTGGAACCTCGGAT 1140	
QY	61 CGATCTACTGTAAATACATCGATTCCTCTCTGTAACTCTAGGTGAAAGT 60	Db	1141 GAGGAGCAGGAGCTGTTGGTCAACCCCTGGATTGCTGTTCAATCACAGGAT 1200	
Db	61 CGATCTACTGTAAATACATCGATTCCTCTCTGTAACTCTAGGTGAAAGT 60	QY	1141 GAGGAGCAGGAGCTGTTGGTCAACCCCTGGATTGCTGTTCAATCACAGGAT 1200	
QY	121 ATTATGGCTTGATAATTAGTAAATGATGATCATGATGTTGGAAATCATAGA 180	Db	1201 AAAGAAGACGGTCACCCAGGGAACTCTACACCTCTTCCAGGTTCTGACC 1260	
Db	121 ATTATGGCTTGATAATTAGTAAATGATGATGTTGGAAATCATAGA 180	QY	1201 AAAGAAGACGGTCACCCAGGGAACTCTACACCTCTTCCAGGTTCTGACC 1260	
QY	181 TCGAATTAATTCGACCAATTCTTATGGTCAACTGAACTGAACTCTGATT 240	Db	1261 TACAGATCTGCTCTAGACCGTATGTTGAACTCTTCTGAACTTCTGATT 1320	
Db	181 TCGAATTAATTCGACCAATTCTTATGGTCAACTGAACTGAACTCTGATT 240	QY	1261 TACAGATCTGCTCTAGACCGTATGTTGAACTCTTCTGAACTTCTGATT 1320	
QY	241 GGATTGGTTCTCGACCAATTCTTATGGTCAACTGAACTGAACTCTGATT 240	Db	1321 ATTGCTCTGTCGCTCATGCTCTGTTACCGTGTGAACTTCTGAACTTCTG 1380	
Db	241 GGATTGGTTCTCGACCAATTCTTATGGTCAACTGAACTGAACTCTGATT 240	QY	1321 ATTGCTCTGTCGCTCATGCTCTGTTACCGTGTGAACTTCTGAACTTCTG 1380	
QY	301 TATAAACAAATATGATAAGAGAGAGGAGATGAACTCTGTTCTGAACTTCTG 360	Db	1381 TACACTCTGGGAAAGATGAGTAACTTCAATGGTAGTGGAGGATGAGGAT 1440	
Db	301 TATAAACAAATATGATAAGAGAGAGGAGATGAACTCTGTTCTGAACTTCTG 360	QY	1381 TACACTCTGGGAAAGATGAGTAACTTCAATGGTAGTGGAGGATGAGGAT 1440	
QY	361 CTCACTATATTCTTGTACTCTACACTGGTACTCTGTTGAGGATGCTAGGAT 420	Db	1441 GAGATCATGGCGAGTTCCATCAGCAAACCCCTCTGGTGTCTTCTGCGTA 1500	
Db	361 CTCACTATATTCTTGTACTCTACACTGGTACTCTGTTGAGGATGCTAGGAT 420	QY	1441 GAGATCATGGCGAGTTCCATCAGCAAACCCCTCTGGTGTCTTCTGCGTA 1500	
QY	421 GAAGAAATTAGGCAAGTACAAGAAAGCAGTGTAAAGTAGTGTGACCTGACTAT 480	Db	1501 GCCCCCTGGCTTACCCCTGTACTATCTCTCTCTCTAGTTCTGCTCTCTCA 1560	
Db	421 GAAGAAATTAGGCAAGTACAAGAAAGCAGTGTAAAGTAGTGTGACCTGACTAT 480	QY	1501 GCCCCCTGGCTTACCCCTGTACTATCTCTCTCTAGTTCTGCTCTCTCA 1560	
QY	481 GCAGCCTGGGAGGATGATCAATATGAAAGAAATTAGAAGAGCTTGGTTTCATG 540	Db	1561 AGAATTCATGGAGCTGTTGCTTGTGTTAGTATGTCATAAGGCTTACCGA 1620	
Db	481 GCAGCCTGGGAGGATGATCAATATGAAAGAAATTAGAAGAGCTTGGTTTCATG 540	QY	1561 AGAATTCATGGAGCTGTTGCTTGTGTTAGTATGTCATAAGGCTTACCGA 1620	
QY	541 GTGACCAATTGGTGTGACCAATTGACAATGCTGCGAGTTTACAATGGTC 600	Db	1621 CGAGCTGTGCTGACATGGATGATGCTGAGCTTCTCTGAGTAGCTGGCTCTATT 1680	
Db	541 GTGACCAATTGGTGTGACCAATTGACAATGCTGCGAGTTTACAATGGTC 600	QY	1621 CGAGCTGTGCTGACATGGATGATGCTGAGCTTCTCTGAGTAGCTGGCTCTATT 1680	
QY	601 ACTCGGAACTGAAAGGGAGAGTGGCTTCAGCAACTACTATGGTTTGTGTT 660	Db	1681 CTTGCAAGCTGAACTCTCAATTACCGTCACTTCTGAGTTCTGAGGAA 1740	
Db	601 ACTCGGAACTGAAAGGGAGAGTGGCTTCAGCAACTACTATGGTTTGTGTT 660	QY	1681 CTTGCAAGCTGAACTCTCAATTACCGTCACTTCTGAGTTCTGAGGAA 1740	
QY	661 GGTAAACCGTCAATAGGACATTCAACAAAGATCGGGTAGATGCGATGCAACTCGGT 720	Db	1741 CTTGCAAGCTGAACTCTCAATTACCGTCACTTCTGAGTTCTGAGGAA 1800	
Db	661 GGTAAACCGTCAATAGGACATTCAACAAAGATCGGGTAGATGCGATGCAACTCGGT 720	QY	1741 CTTGCAAGCTGAACTCTCAATTACCGTCACTTCTGAGTTCTGAGGAA 1800	
QY	721 AAACAAAGGTGCAAGGCGCATTTGTCAGCTGGGCGCGTGGACGATGATCATGATGAA 780	Db	1801 ATGCTGCTCACTTGCCCTGAGCTCTCTTCTGAGTAGTGTGAACTCTGAG 1920	
Db	721 AAACAAAGGTGCAAGGCGCATTTGTCAGCTGGGCGCGTGGACGATGATCATGATGAA 780	QY	1801 ATGCTGCTCACTTGCCCTGAGCTCTCTTCTGAGTAGTGTGAACTCTGAG 1920	
QY	781 GATGTTTACTCTGGGAGATGTTGAGTGTGATGATGATGATGATGATGATGATGAAAT 840	Db	1861 TCTATTATGAGAGCAACTAACACTCTGGAACAGGAGGAAATTCCGGCTAGTT 1920	
Db	781 GATGTTTACTCTGGGAGATGTTGAGTGTGATGATGATGATGATGATGATGAAAT 840	QY	1861 TCTATTATGAGAGCAACTAACACTCTGGAACAGGAGGAAATTCCGGCTAGTT 1920	

